RECEIVED
CENTRAL FAX CENTER
APR 29 2004

OFFICIAL

SYRRX

FACSIMILE TRANSMITTAL SHEET

TO: COMMISSIONER FOR PATENTS	From: DAVID WEITZ, REG. NO. 38,362
FAX NUMBER: (703) 872-9306	DATE: APRIL 27, 2004
COMPANY: U.S. PATENT AND TRADEMARK OFFICE	TOTAL NO. OF PAGES INCLUDING COVER: 12
PHONE NUMBER:	SENDER'S PHONE NUMBER: (858) 731-3508
RE: U.S. APPLICATION SERIAL NO. 09/848,866 – RESPONSE TO RESTRICTION REQUIREMENT	SENDER'S FAX NUMBER: (858) 550-0992

☐ URGENT ☐ FOR REVIEW ☐ PLEASE COMMENT ☐ PLEASE REPLY ☐ PLEASE RECYCLE

NOTES/COMMENTS:

10410 SCIENCE CENTER DRIVE • SAN DIEGO, CA 92121
PHONE: (858) 731-3508 • FAX: (858) 550-0992

PTO/SB/21 (05-03)
Approved for use through 04/30/2003. OMB 0651-0031
U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE
Under the Paper Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

TRANSMITTAL FORM (to be used for all correspondence after initial filing)			
		Application Number	09/848,866
		Filing Date	May 4, 2001
		First Named Inventor	Duncan McRae et al.
		Art Unit	1631
		Examiner Name	Michael L. Borin
Total Number of Pages in This Submission	11	Attorney Docket Number	SYRTECH-5001-U

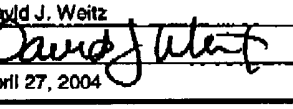
ENCLOSURES *(check all that apply)*

- [ ] Fee Transmittal Form
  - [ ] Fee Attached
- [X] Amendment / Reply
  - [ ] After Final
  - [ ] Affidavits/declaration(s)
- [ ] Extension of Time Request
- [ ] Express Abandonment Request
- [ ] Information Disclosure Statement
- [ ] Certified Copy of Priority Document(s)
- [ ] Response to Missing Parts/ Incomplete Application
  - [ ] Response to Missing Parts under 37 CFR 1.52 or 1.53
- [ ] Drawing(s)
- [ ] Licensing-related Papers
- [ ] Petition
- [ ] Petition to Convert to a Provisional Application
- [ ] Power of Attorney, Revocation Change of Correspondence Address
- [ ] Terminal Disclaimer
- [ ] Request for Refund
- [ ] CD, Number of CD(s) _____
- [ ] After Allowance communication to Group
- [ ] Appeal Communication to Board of Appeals and Interferences
- [ ] Appeal Communication to Group **(Appeal Notice, Brief, Reply Brief)**
- [ ] Proprietary Information
- [ ] Status Letter
- [ ] Other Enclosure(s) *(please identify below):*

Remarks

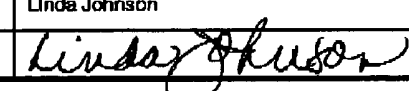
Although Applicants do not believe any fees are required, the Commissioner is authorized to charge any fees required by the filing of these papers to Syrrx's Deposit Account No. **50-2256.**

SIGNATURE OF APPLICANT, ATTORNEY, OR AGENT

Firm or Individual name	Syrrx, Inc. David J. Weitz
Signature	
Date	April 27, 2004

CERTIFICATE OF TRANSMISSION/MAILING

I hereby certify that this correspondence is being facsimile transmitted **(703) 872-9306** to the USPTO or deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450 on the date shown below.

Type or printed	Linda Johnson		
Signature		Date	April 27, 2004

This collection of information is required by 37 CFR 1.5. The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.14. This collection is estimated to take 12 minutes to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. **SEND TO: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.**

If you need assistance in completing the form, call 1-800-PTO-9199 (1-800-786-9199) and select option 2.

U.S. Application Serial No. 09/848,866 Docket No. SYRTECH-5001-U
Response to Office Action dated April 27, 2004
Office Action Mailed April 20, 2004

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of)
)
Duncan McRee et al.) Group Art Unit: 1631
)
Application No.: 09/848,866) Examiner: Borin, Michael L.
)
Filed: May 4, 2001)
)
Title: DETERMINING STRUCTURES)
BY PERFORMING)
COMPARISONS BETWEEN)
MOLECULAR REPLACEMENT)
RESULTS FOR MULTIPLE)
DIFFERENT BIOMOLECULES)
)

RESPONSE TO RESTRICTION AS TO SPECIES

Mail Stop Non-Fee Amendment
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

In response to Examiner's Restriction Requirement mailed April 20, 2004, Applicants respectfully request reconsideration of the above-referenced application in view of the following election, amendment, and remarks.

AMENDED SECTIONS

X **Claims** appear at pages 2-8

REMARKS/ARGUMENTS

X **Remarks / Arguments** appear at page 9

This listing of claims will replace all prior versions and listings of claims in the application.

LISTING OF CLAIMS

1. (original) A method for identifying a search model to use in molecular replacement for determining a structure of a target biomolecule from crystal data, the method comprising:

employing computer executable logic to perform multiple molecular replacement searches on crystal data of the target biomolecule where a group of different biomolecule structures are used as search models for the multiple molecular replacement searches; and

employing computer executable logic to compare solutions from the multiple molecular replacement searches, the comparison producing data from which biomolecule structures in the group can be identified as having superior structural identity with the target biomolecule as compared to the other biomolecule structures in the group.

2. (original) A method according to claim 1 wherein comparing molecular replacement solutions comprises comparing figures of merit calculated for the molecular replacement solutions.

3. (currently amended) A method according to claim ~~1~~ 2 wherein comparing molecular replacement solutions comprises performing a statistical analysis on figures of merit calculated for the molecular replacement solutions.

4. (currently amended) A method according to claim ~~1~~ 2 wherein comparing molecular replacement solutions comprises determining which of the biomolecule structures in the group produced a molecular replacement solution whose figure of merit is at least two standard deviations better than the average figure of merit for molecular replacement solutions for the biomolecule structures in the group.

5. (currently amended) A method according to claim ~~1~~ 2 wherein comparing molecular replacement solutions comprises determining which of the biomolecule structures in the group produced a molecular replacement solution whose figure of merit is at least three standard deviations better than the average figure of merit for molecular replacement solutions for the biomolecule structures in the group.

6. (currently amended) A method according to claim ~~1~~ 2 wherein comparing molecular replacement solutions comprises determining which of the biomolecule structures in the group produced a molecular replacement solution whose figure of merit is at least five standard deviations better than the average figure of merit for molecular replacement solutions for the biomolecule structures in the group.

7. (currently amended) A method according to claim ~~1~~ 2 wherein comparing molecular replacement solutions comprises determining which of the biomolecule structures in the group produced a molecular replacement solution whose figure of merit is at least ten standard deviations better than the average figure of merit for molecular replacement solutions for the biomolecule structures in the group.

8. (original) A method according to claim 1 wherein comparing molecular replacement solutions comprises comparing root mean square errors for each molecular replacement solution of a probability-weighted average over all possible phase choices.

9. (original) A method according to claim 1 wherein comparing molecular replacement solutions comprises establishing a background correlation level between the biomolecule structures in the group and the target biomolecule based on the molecular replacement solutions and determining which of the biomolecule structures in the group produced a molecular replacement solution that exceeds the background correlation level by at least two standard deviations.

10. (original) A method according to claim 1 wherein comparing molecular replacement solutions comprises establishing a background correlation level between the biomolecule structures in the group and the target biomolecule based on the molecular replacement solutions and determining which of the biomolecule structures in the group produced a molecular replacement solution that exceeds the background correlation level by at least three standard deviations.

11. (original) A method according to claim 1 wherein comparing molecular replacement solutions comprises establishing a background correlation level between the biomolecule structures in the group and the target biomolecule based on the molecular replacement solutions and determining which of the biomolecule structures in the group produced a molecular replacement solution that exceeds the background correlation level by at least five standard deviations.

12. (original) A method according to claim 1 wherein comparing molecular replacement solutions comprises establishing a background correlation level between the biomolecule structures in the group and the target biomolecule based on the molecular replacement solutions and determining which of the biomolecule structures in the group produced a molecular replacement solution that exceeds the background correlation level by at least ten standard deviations.

13. (currently amended) A method according to claim ~~1~~ 2 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least 3 different biomolecule structures.

14. (currently amended) A method according to claim ~~1~~ 2 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least 0.1% of the protein structures stored in the Protein Data Bank.

15. (currently amended) A method according to claim ~~1~~ 2 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least one biomolecule structure that has less than 70% sequence identity with the target biomolecule.

16. (currently amended) A method according to claim ~~1~~ 2 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least two different biomolecule structures that are structurally dissimilar to each other.

17. (currently amended) A method according to claim ~~1~~ 2 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least two different biomolecule structures that have less than 70% sequence identity with each other.

18. (currently amended) A method according to claim ~~1~~ 2 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least one predicted structure for a biomolecule.

19. (currently amended) A method according to claim ~~1~~ 2 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least one structure where at least a portion of the native structure has been removed.

20. (currently amended) A method according to claim ~~1~~ 2 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least one structure which comprises a combination of two or more structure fragments.

21-51 (withdrawn)

52. (original) A computer readable medium useful in association with a computer which includes a processor and a memory, the computer readable medium comprising:

logic for performing multiple molecular replacement searches on crystal data of a target biomolecule where a group of different biomolecule structures are used as search models for the multiple molecular replacement searches; and

logic for comparing solutions from the multiple molecular replacement searches, the comparison producing data from which biomolecule structures from the group can be identified as having superior structural identity with the target biomolecule as compared to the other biomolecule structures in the group.

53. (original) A method for identifying a search model to use in molecular replacement for determining a structure of a target biomolecule from crystal data, the method comprising:

employing computer executable logic to perform multiple molecular replacement searches on crystal data of the target biomolecule where a group of different biomolecule structures are used as search models for the multiple molecular replacement searches; and

employing computer executable logic to identify a biomolecule structure from the group whose use as a search model produces a molecular replacement solution that is superior to the molecular replacement solutions produced by the other biomolecule structures in the group.

54. (original) A computer readable medium useful in association with a computer which includes a processor and a memory, the computer readable medium comprising:

logic for performing multiple molecular replacement searches on X-ray diffraction data of a target biomolecule where a group of different biomolecule structures are used as search models for the multiple molecular replacement searches; and

logic for identifying a biomolecule structure from the group whose use as a search model produces a molecular replacement solution that is superior to the

molecular replacement solutions produced by the other biomolecule structures in the group.

55. (original) A method for determining a structure of a target biomolecule from crystal data, the method comprising:

employing computer executable logic to perform multiple molecular replacement searches on crystal data of the target biomolecule where a group of different biomolecule structures are used as search models for the multiple molecular replacement searches;

employing computer executable logic to identify a biomolecule structure from the group whose use as a search model produces a molecular replacement solution that is superior to the molecular replacement solutions produced by the other biomolecule structures in the group; and

employing computer executable logic to determine a structure for the target biomolecule employing the identified biomolecule structure.

56. (original) A computer readable medium useful in association with a computer which includes a processor and a memory, the computer readable medium comprising:

logic for performing multiple molecular replacement searches on crystal data of a target biomolecule where a group of different biomolecule structures are used as search models for the multiple molecular replacement searches;

logic for identifying a biomolecule structure from the group whose use as a search model produces a molecular replacement solution that is superior to the molecular replacement solutions produced by the other biomolecule structures in the group; and

logic for determining a structure for the target biomolecule employing the identified biomolecule structure.

57. (original) A method for identifying a search model to use in molecular replacement for determining a structure of a target biomolecule from crystal data, the method comprising:

(a) employing computer executable logic to perform multiple molecular replacement searches on crystal data of the target biomolecule using multiple different biomolecule structures as search models;

(b) employing computer executable logic to compare the resulting molecular replacement solutions in order to identify a biomolecule structure whose use as a search model produces a molecular replacement solution that is superior to the molecular replacement solutions of other biomolecule structures upon which the molecular replacement searches were performed; and

(c) if none of the molecular replacement solutions are comparatively better, evaluating additional biomolecule structures by repeating steps (a) and (b) with the additional biomolecule structures until a biomolecule structure is identified which produces a molecular replacement solution that is superior to the molecular replacement solutions of other biomolecule structures upon which the molecular replacement searches were performed.

REMARKS/ARGUMENTS

The Examiner has issued a restriction requirement alleging that the application claims eight distinct species. Claims 1 and 52-57 were indicated as being generic.

Pursuant to 37 C.F.R. § 1.142, Applicants elect the species directed to determining molecular replacement solutions. Claims 2-12 are directed to this species. Claims 13-20 have been amended to depend from claim 2 and thus now fall within the elected species.

Claims 21-51 are withdrawn as being directed to the non-elected species pursuant to 37 C.F.R. 1.142(b). However, Applicants reserve the right pursuant to 37 C.F.R. § 1.141 to pursue claims to the non-elected species in this application in the event that a generic claim is found to be allowable.

Applicants also reserve the right pursuant to 35 U.S.C. § 121 to file one or more divisional applications directed to the non-elected species during the pendency of the present application.

CONCLUSION

Applicants earnestly believe that they are entitled to a letters patent, and respectfully solicit the Examiner to expedite prosecution of this patent application to issuance. Should the Examiner have any questions, the Examiner is encouraged to telephone the undersigned.

Respectfully submitted,
Syrrx, Inc.

Dated: April 27, 2004

By: _____
David J. Weitz, General Counsel
& V. P. of Intellectual Property
Reg. No. 38,362

Customer No. 32793
Syrrx, Inc.
10410 Science Center Drive
San Diego, CA 92121
Telephone: (858) 622-8528
Facsimile: (858) 550-0992